EXHIBIT A

VERSION OF SPECIFICATION WITH MARKINGS TO SHOW CHANGES MADE

U.S. Patent Application Serial No. 09/602,833

Page 13, lines 28 to page 14, line 19:

The invention encompasses highly related gene homologs of the SGT4 encoding polynucleotide sequences described above. Highly related gene homologs are polynucleotides encoding proteins that are at least 30% identical, or at least 40% identical, preferably 50% identical, more preferably 60% identical, even more preferably 70% or even 80% identical, and most preferably 90% identical, at the amino acid level to the disclosed SGT4 proteins. Percent similarity may be determined, for example, by comparing sequence information using the BLAST computer program, version 2.0, available on the World-Wide Web [at http://www.ncbinlm.nih.gov]. For a description of BLAST, *see* Altschul *et al.*, *J. Mol. Biol.* **215**:403-10 (1990); Altschul *et al.*, *Nucleic Acids Res.* **25**:3389-3402 (1997). Typical parameters for determining the similarity of two sequences using BLAST 2.0 are a reward for match of 1, penalty for mismatch of -2, open gap and extension gap penalties of 5 and 2, respectively, a gap dropoff of 50, and a word size of 11. Highly related homologs can encode proteins sharing functional activities with SGT4. Other gene homologs are those genes that encode proteins having 100% identity with SGT4 over 6 consecutive amino acids, and more preferably 8 amino acids, yet more preferably 15 amino acids, or even 20 amino acids. Alternatively, percent homology may be determined using the GAP computer program, version 6.0 described by Devereux *et al.*, *Nucl. Acids. Res.*, 12:387 (1984). The GAP program utilizes the alignment method of Neeldeman and Wunsch, *J. Mol. Biol.* 48:443 (1970), as revised by Smith and Waterman, *Adv. Appl. Math*, 2:482 (1970). Percent similarity may be determined, for example, by comparing sequence information using the BLAST computer program, version 2.0, available on the World-Wide Web [at http://www.ncbi.nlm.nih.gov].

Page 28, lines 4-18:

In the fourth approach, the expression of the SGT4 protein product can be assessed immunologically, for example by Western blots, immunoassays such as radioimmuno-precipitation, enzyme-linked immunoassays and the like. This can be achieved by using an anti-SGT4 antibody. Expression of the SGT4 protein product can also be assessed using analytical techniques such as amino acid sequencing, which can be accomplished by means of, for example, Edman degradation or tandem mass spectroscopy, or by analysis of the

masses of peptides generated by partial hydrolysis of the protein product using mass spectroscopy. In the identification of SGT4 protein by mass spectroscopy, it will often be desirable to separate the SGT4 protein from other protein constituents of the cell by means of two-dimensional gel electrophoresis, partially hydrolyze the isolated protein using an amino acid specific protease (*e.g.*, Lys-C, trypsin), and then determine the mass of the resulting peptide fragments using mass spectroscopy. Determination of peptide mass can then be used to identify the protein as SGT4, or a variant thereof, using a database of the predicted masses of protein proteolysis products and analysis software such as Protein Prospector, which is publicly available on the internet [at http://prospector.ucsf.edu].